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 ccattacgac gagggcgtca ggatgggctc tctgggcctc ttcctgcagt gcgccatcag 1020
 tctggtgttc tctctgggtga tggaccggct ggtgcagcgc ttcggcaccg gggccgtgta 1080
 cctcgctct gtggcggtt tccccgtcgc cgcggcgcg acctgctgt ctcatctgt 1140
 cgccgtgggtg accgccagcg ccgcctgac cggcttcacc ttcagtgcgc tccagattct 1200
 10 gccctacacc ctggcgctc tgtaccatcg cgagaagcag gtgttcctgc ccaagtaccg 1260
 cggggacaca gggggagctt cctctgagga cagcctgatg accagcttct tgcccggccc 1320
 caagccgggg gcccctttcc ccaacggcca tgtcggggcg ggcggcagcg gcctgtctcc 1380
 tccccccccc gccctgtgcg gcgctagtgc ctggcagctg agcgtgcggg tgggtggtggg 1440
 ggagccacc gaggttaggg tcgtgcctgg ccgggggacg tgccctggacc tggccatcct 1500
 15 cgactccgcc ttcctgctct ccaggtggc gccagcctg ttcattggga gtatcgtgca 1560
 gctgagccag agcgtgaccg cctacatggt gagcgccgc ggccgtgggt tgggtggccat 1620
 ctactttgcc acccaggtcg tgttcgacaa gagcgatctc gccaaagtata gcgcctgact 1680
 cgaggcag 1688

20 <210> 23
 <211> 435
 <212> DNA
 <213> Artificial Sequence

25 <220>
 <223> Hybrid gene between St. pneum. C-LytA, P2 T helper
 epitope and a small portion of the 5' end of human
 P501S

30 <400> 23
 atggcggccg cttacgtaca ttccgacggc tcttatccaa aagacaagtt tgagaaaatc 60
 aatggcactt ggtactactt tgacagttca ggctatatgc ttgcagaccg ctggagggaag 120
 cacacagacg gcaactggta ctggttcgac aactcaggcg aaatggctac aggctggaag 180
 aaaatcgctg ataagtggta ctatttcaac gaagaagggtg ccatgaagac aggctgggtc 240
 35 aagtacaagg acacttggtg ctacttagac gctaaagaag gcgccatgca atacatcaag 300
 gctaactcta agttcattgg tatcactgaa ggcgtcatgg tatcaaatgc ctttatccag 360
 tcagcgggacg gaacaggctg gtactacctc aaaccagacg gaacactggc agacaggcca 420
 gaaaagttca tgtac 435

40 <210> 24
 <211> 435
 <212> DNA
 <213> Artificial Sequence

45 <220>
 <223> Hybrid gene between St. pneum. C-LytA, P2 T helper
 epitope and a small portion of the 5' end of human
 P501S - codon-optimised

50 <400> 24
 atggcggccc cctacgtgca tagcgacggg agctacccca aggacaagtt cgagaagatc 60
 aacgggacat ggtactactt cgactcctcc ggctacatgc tcgccgaccg ctggcggaag 120
 cacaccgacg gcaactggta ctggttcgat aactcgggag agatggccac cggctggaag 180
 aagatcgcgg acaagtggta ctatttcaac gaggagggcg ccatgaagac cggctgggtg 240
 55 aagtataagg acacctggta ctacctgac gccaaaggag gcgccatgca gtatatcaag 300
 gccaacagca agttcatcgg catcaccgag ggagtgatgg tcagcaacgc ctttatccag 360
 agcggcgacg gcaccgatg gtactacttg aagccggacg gcaccctcgc ggatcgggcc 420
 gagaagttca tgtac 435

60 <210> 25
 <211> 435

<212> DNA
 <213> Artificial Sequence

<220>
 5 <223> Hybrid gene between St. pneum. C-LytA, P2 T helper epitope and a small portion of the 5' end of human P501S - codon-optimised

<400> 25
 10 atggccgccc cctacgtgca cagcgacggg tcctacccaa aggacaagtt cgagaagatc 60
 aacggcacgt ggtactatct cgacagcagc ggctacatgc tcgccgatcg ctggcgcaag 120
 cacaccgacg ggaactggta ctggttcgac aactctggcg agatggctac ggggtggaag 180
 aagatcgccg acaagtggta ctacttcaac gaggagggcg ccatgaagac cgggtgggtg 240
 aagtacaagg acacctggta ctacctggac gctaaggagg gcgccatgca gtacatcaag 300
 15 gccaaactga agttcatcgg gatcaccgag ggcgtgatgg tcagtaacgc ttatcatccag 360
 agcgcggacg gcacaggctg gtattacctg aagcccgatg gcaccctggc ggacagacct 420
 gagaaattca tgtac 435

<210> 26
 20 <211> 464
 <212> DNA
 <213> Artificial Sequence

<220>
 25 <223> Hybrid gene between St. pneum. C-LytA, P2 T helper epitope and a small portion of the 5' end of human P501S - codon-optimised

<400> 26
 30 gacggctagc gccaccatgg ccgcccgccta cgtgcatagc gacgggagct accccaagga 60
 caagttcgag aagatcaacg ggacatggta ctacttcgac tcctccggct acatgctcgc 120
 cgaccgctgg cggaagcaca ccgacggcaa ctggtactgg ttcgataact cgggagagat 180
 ggccaccggc tggaagaaga tcgcggaaca gtggtactat ttcaacgagg agggcgccat 240
 gaagaccggc tgggtgaagt ataaggacac ctggtactac ctcgacgcca aggagggcgc 300
 35 catgcagtat atcaaggcca acagcaagtt catcggcac accgagggag tgatggtcag 360
 caacgccttt atccagagcg ccgacggcac cggatggtac tacttgaagc cggacggcac 420
 cctcgccgat cggcccgaga agttcatgta ctgactcgag gcag 464

<210> 27
 40 <211> 652
 <212> PRT
 <213> Artificial Sequence

<220>
 45 <223> Hybrid protein between St. pneum. C-LytA, P2 T helper epitope and amino acids 51-553 of human P501S

<400> 27
 50 Met Ala Ala Ala Tyr Val His Ser Asp Gly Ser Tyr Pro Lys Asp Lys
 1 5 10 15
 Phe Glu Lys Ile Asn Gly Thr Trp Tyr Tyr Phe Asp Ser Ser Gly Tyr
 20 25 30
 Met Leu Ala Asp Arg Trp Arg Lys His Thr Asp Gly Asn Trp Tyr Trp
 35 40 45
 55 Phe Asp Asn Ser Gly Glu Met Ala Thr Gly Trp Lys Lys Ile Ala Asp
 50 55 60
 Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala Met Lys Thr Gly Trp Val
 65 70 75 80
 60 Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp Ala Lys Glu Gly Ala Met
 85 90 95

	Gln	Tyr	Ile	Lys	Ala	Asn	Ser	Lys	Phe	Ile	Gly	Ile	Thr	Glu	Gly	Val
				100					105					110		
	Met	Val	Ser	Asn	Ala	Phe	Ile	Gln	Ser	Ala	Asp	Gly	Thr	Gly	Trp	Tyr
			115					120					125			
5	Tyr	Leu	Lys	Pro	Asp	Gly	Thr	Leu	Ala	Asp	Arg	Pro	Glu	Lys	Phe	Met
		130					135					140				
	Tyr	Met	Val	Leu	Gly	Ile	Gly	Pro	Val	Leu	Gly	Leu	Val	Cys	Val	Pro
	145					150					155				160	
	Leu	Leu	Gly	Ser	Ala	Ser	Asp	His	Trp	Arg	Gly	Arg	Tyr	Gly	Arg	Arg
				165						170					175	
10	Arg	Pro	Phe	Ile	Trp	Ala	Leu	Ser	Leu	Gly	Ile	Leu	Leu	Ser	Leu	Phe
			180						185					190		
	Leu	Ile	Pro	Arg	Ala	Gly	Trp	Leu	Ala	Gly	Leu	Leu	Cys	Pro	Asp	Pro
			195					200					205			
15	Arg	Pro	Leu	Glu	Leu	Ala	Leu	Leu	Ile	Leu	Gly	Val	Gly	Leu	Leu	Asp
		210					215					220				
	Phe	Cys	Gly	Gln	Val	Cys	Phe	Thr	Pro	Leu	Glu	Ala	Leu	Leu	Ser	Asp
	225					230					235					240
	Leu	Phe	Arg	Asp	Pro	Asp	His	Cys	Arg	Gln	Ala	Tyr	Ser	Val	Tyr	Ala
				245						250					255	
20	Phe	Met	Ile	Ser	Leu	Gly	Gly	Cys	Leu	Gly	Tyr	Leu	Leu	Pro	Ala	Ile
			260						265					270		
	Asp	Trp	Asp	Thr	Ser	Ala	Leu	Ala	Pro	Tyr	Leu	Gly	Thr	Gln	Glu	Glu
			275					280					285			
25	Cys	Leu	Phe	Gly	Leu	Leu	Thr	Leu	Ile	Phe	Leu	Thr	Cys	Val	Ala	Ala
		290					295					300				
	Thr	Leu	Leu	Val	Ala	Glu	Glu	Ala	Ala	Leu	Gly	Pro	Thr	Glu	Pro	Ala
	305					310					315				320	
	Glu	Gly	Leu	Ser	Ala	Pro	Ser	Leu	Ser	Pro	His	Cys	Cys	Pro	Cys	Arg
				325						330					335	
30	Ala	Arg	Leu	Ala	Phe	Arg	Asn	Leu	Gly	Ala	Leu	Leu	Pro	Arg	Leu	His
			340						345					350		
	Gln	Leu	Cys	Cys	Arg	Met	Pro	Arg	Thr	Leu	Arg	Arg	Leu	Phe	Val	Ala
			355					360						365		
35	Glu	Leu	Cys	Ser	Trp	Met	Ala	Leu	Met	Thr	Phe	Thr	Leu	Phe	Tyr	Thr
		370					375					380				
	Asp	Phe	Val	Gly	Glu	Gly	Leu	Tyr	Gln	Gly	Val	Pro	Arg	Ala	Glu	Pro
	385					390					395					400
	Gly	Thr	Glu	Ala	Arg	Arg	His	Tyr	Asp	Glu	Gly	Val	Arg	Met	Gly	Ser
				405						410					415	
40	Leu	Gly	Leu	Phe	Leu	Gln	Cys	Ala	Ile	Ser	Leu	Val	Phe	Ser	Leu	Val
				420					425					430		
	Met	Asp	Arg	Leu	Val	Gln	Arg	Phe	Gly	Thr	Arg	Ala	Val	Tyr	Leu	Ala
			435					440					445			
45	Ser	Val	Ala	Ala	Phe	Pro	Val	Ala	Ala	Gly	Ala	Thr	Cys	Leu	Ser	His
		450					455					460				
	Ser	Val	Ala	Val	Val	Thr	Ala	Ser	Ala	Ala	Leu	Thr	Gly	Phe	Thr	Phe
	465					470					475					480
	Ser	Ala	Leu	Gln	Ile	Leu	Pro	Tyr	Thr	Leu	Ala	Ser	Leu	Tyr	His	Arg
				485						490					495	
50	Glu	Lys	Gln	Val	Phe	Leu	Pro	Lys	Tyr	Arg	Gly	Asp	Thr	Gly	Gly	Ala
				500					505					510		
	Ser	Ser	Glu	Asp	Ser	Leu	Met	Thr	Ser	Phe	Leu	Pro	Gly	Pro	Lys	Pro
			515					520					525			
55	Gly	Ala	Pro	Phe	Pro	Asn	Gly	His	Val	Gly	Ala	Gly	Gly	Ser	Gly	Leu
		530					535					540				
	Leu	Pro	Pro	Pro	Pro	Ala	Leu	Cys	Gly	Ala	Ser	Ala	Cys	Asp	Val	Ser
	545					550					555					560
	Val	Arg	Val	Val	Val	Gly	Glu	Pro	Thr	Glu	Ala	Arg	Val	Val	Pro	Gly
				565						570					575	
60	Arg	Gly	Ile	Cys	Leu	Asp	Leu	Ala	Ile	Leu	Asp	Ser	Ala	Phe	Leu	Leu

580 585 590
 Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser Ile Val Gln Leu Ser
 595 600 605
 Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala Gly Leu Gly Leu Val
 610 615 620
 5 Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp Lys Ser Asp Leu Ala
 625 630 635 640
 Lys Tyr Ser Ala Gly Gly His His His His His
 645 650
 10
 <210> 28
 <211> 1959
 <212> DNA
 15 <213> Artificial Sequence
 <220>
 <223> DNA encoding the Hybrid protein between St. pneum.
 C-LytA, P2 T helper epitope and amino acids 51-553
 20 of human P501S
 <400> 28
 atggcgccg cttacgtaca ttccgacggc tcttatccaa aagacaagtt tgagaaaatc 60
 aatggcactt ggtactactt tgacagttca ggctatatgc ttgcagaccg ctggaggaag 120
 25 cacacagacg gcaactggta ctggttcgac aactcaggcg aaatggctac aggctggaag 180
 aaaatcgctg ataagtggta ctatttcaac gaagaagggtg ccatgaagac aggtcgggtc 240
 aagtacaagg acacttggta ctacttagac gctaaagaag gcgccatgca atacatcaag 300
 gctaaactcta agttcattgg tactactgaa ggctcatggt tatcaaatgc ctttatccag 360
 tcagcggacg gaacaggctg gtactacctc aaaccagacg gaacactggc agacaggcca 420
 30 gaaaagtcca tgtacatggt gctgggcatt ggtccagtgc tgggcctggg ctgtgtcccg 480
 ctcttaggct cagccagtga ccactggcgt ggacgctatg gccgcgcgcg gcccttcac 540
 tgggcactgt ccttgggcat cctgctgagc ctctttctca tcccaaggcg cggctgggta 600
 gcagggctgc tgtgcccgga tcccaggccc ctggagctgg cactgctcat cctgggctgt 660
 gggctgctgg acttctgtgg ccagggtgag ttactccac tggaggccct gctctctgag 720
 35 ctcttcgggg acccggaaca ctgtcgcctg gcctactctg tctatgcctt catgatcagt 780
 cttgggggct gcctgggcta cctctgcct gccattgact gggacaccag tggcctggcc 840
 ccctacctgg gacccagga ggagtgcttc tttggcctgc tcaccctcat cttcctcacc 900
 tgcgtagcag ccacactgct ggtggctgag gaggcagcgc tgggccccac cgagccagca 960
 gaagggtgtg cggccccctc ctgtgcgcc cactgctgtc catgcccggg ccgcttggtt 1020
 40 ttccggaacc tgggcgccc gcttccccgg ctgcaccagc tgtgctgccc catgccccgc 1080
 accctgcgcc ggctcttcgt ggctgagctg tgcagctgga tggcactcat gaccttcacg 1140
 ctgttttaca cggatttcgt gggcgagggg ctgtaccagg gcgtgcccag agctgagccg 1200
 ggcaccgagg cccggagaca ctatgatgaa ggcttcgga tgggcagcct ggggctgttc 1260
 ctgcagtgcg ccattctcct ggtcttctct ctggtcatgg accggctggg gcagcgattc 1320
 45 ggcactcgag cagtctatct ggccagtgtg gcagctttcc ctgtggctgc cgggtgccaca 1380
 tgcctgtccc acagtgtggc cgtggtgaca gcttcagccg ccctcaccgg gttcaccttc 1440
 tcagccctgc agatcctgcc ctacacactg gcctccctct accaccggga gaagcagggt 1500
 ttctgcccc aataccgagg ggacactgga ggtgctagca gtgaggacag cctgatgacc 1560
 agcttcctgc caggccctaa gcctggagct cccttcctta atggacacgt ggggtgctgga 1620
 50 ggcagtggcc tgctcccacc tccaccgcg ctctgcgggg cctctgcctg tgatgtctcc 1680
 gtacgtgtgg ttgtgggtga gcccaccgag gccagggtgg ttccgggccc gggcatctgc 1740
 ctggacctgc ccattcctga tagtgcttcc ctgctgtccc aggtggcccc atccctgttt 1800
 atgggtccca ttgtccagct cagccagtct gtcactgcct atatggtgtc tgccgcaggc 1860
 ctgggtctgg tggccattta ctttgttaca caggtagtat ttgacaagag cgacttggcc 1920
 55 aaatactcag cgggtggaca ccatcaccat caccattaa 1959
 <210> 29
 <211> 507
 <212> PRT
 60 <213> Artificial Sequence

<220>

<223> Human P501S (amino acids 55-553) fused to 6 histidine residues

5 <400> 29
Met Val Leu Gly Ile Gly Pro Val Leu Gly Leu Val Cys Val Pro Leu
1 5 10 15
Leu Gly Ser Ala Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg
20 25 30
10 Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile Leu Leu Ser Leu Phe Leu
35 40 45
Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu Leu Cys Pro Asp Pro Arg
50 55 60
15 Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly Val Gly Leu Leu Asp Phe
65 70 75 80
Cys Gly Gln Val Cys Phe Thr Pro Leu Glu Ala Leu Leu Ser Asp Leu
85 90 95
Phe Arg Asp Pro Asp His Cys Arg Gln Ala Tyr Ser Val Tyr Ala Phe
100 105 110
20 Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr Leu Leu Pro Ala Ile Asp
115 120 125
Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu Glu Cys
130 135 140
Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu Thr Cys Val Ala Ala Thr
145 150 155 160
25 Leu Leu Val Ala Glu Glu Ala Ala Leu Gly Pro Thr Glu Pro Ala Glu
165 170 175
Gly Leu Ser Ala Pro Ser Leu Ser Pro His Cys Cys Pro Cys Arg Ala
180 185 190
30 Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu Leu Pro Arg Leu His Gln
195 200 205
Leu Cys Cys Arg Met Pro Arg Thr Leu Arg Arg Leu Phe Val Ala Glu
210 215 220
Leu Cys Ser Trp Met Ala Leu Met Thr Phe Thr Leu Phe Tyr Thr Asp
225 230 235 240
35 Phe Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro Gly
245 250 255
Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg Met Gly Ser Leu
260 265 270
40 Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu Val Phe Ser Leu Val Met
275 280 285
Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr Leu Ala Ser
290 295 300
Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys Leu Ser His Ser
305 310 315 320
45 Val Ala Val Val Thr Ala Ser Ala Ala Leu Thr Gly Phe Thr Phe Ser
325 330 335
Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala Ser Leu Tyr His Arg Glu
340 345 350
50 Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly Asp Thr Gly Gly Ala Ser
355 360 365
Ser Glu Asp Ser Leu Met Thr Ser Phe Leu Pro Gly Pro Lys Pro Gly
370 375 380
Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly Gly Ser Gly Leu Leu
385 390 395 400
55 Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser Ala Cys Asp Val Ser Val
405 410 415
Arg Val Val Val Gly Glu Pro Thr Glu Ala Arg Val Val Pro Gly Arg
420 425 430
60 Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp Ser Ala Phe Leu Leu Ser
435 440 445

Gln Val Ala Pro Ser Leu Phe Met Gly Ser Ile Val Gln Leu Ser Gln
 450 455 460
 Ser Val Thr Ala Tyr Met Val Ser Ala Ala Gly Leu Gly Leu Val Ala
 465 470 475 480
 5 Ile Tyr Phe Ala Thr Gln Val Val Phe Asp Lys Ser Asp Leu Ala Lys
 485 490 495
 Tyr Ser Ala Gly His His His His His His
 500 505

10 <210> 30
 <211> 1524
 <212> DNA
 <213> Artificial Sequence

15 <220>
 <223> DNA encoding Human P501S (amino acids 55-553)
 fused to 6 histidine residues

20 <400> 30
 atggtgctgg gcattggtcc agtgctgggc ctggtctgtg tcccgtctct aggetcagcc 60
 agtgaccact ggcgtggacg ctatggccgc cgccggccct tcatctgggc actgtccttg 120
 ggcacacctgc tgagcctctt tctcatccca agggccggct ggctagcagg gctgctgtgc 180
 ccgcatccca ggcacctgga gctggcactg ctcatcctgg gcgtggggct gctggacttc 240
 25 tgtggccagg tgtgtctcac tccactggag gccctgtctt ctgacctctt ccgggaccgc 300
 gaccactgtc gccaggccta ctctgtctat gccttcatga tcagtcttgg gggctgcctg 360
 ggctacctcc tgccctgcat tgactgggac accagtgcct tggcccccta cctgggcacc 420
 caggaggagt gcctctttgg cctgctcacc ctcatcttcc tcacctgcgt agcagccaca 480
 ctgctgggtgg ctgaggaggc agcgtggggc cccaccgagc cagcagaagg gctgtcggcc 540
 30 ccttccttgt cgccccactg ctgtccatgc cgggcccgc tggctttccg gaacctgggc 600
 gccctgcttc ccggctgca ccagctgtgc tgccgcatgc cccgcacct gcgccggctc 660
 ttcgtggctg agctgtgcag ctggatggca ctcatgacct tcacgtgtt ttacacggat 720
 ttcgtgggctg aggggctgta ccaggcgctg ccagagctg agccgggcac cgaggcccgc 780
 agacactatg atgaaggcgt tcggatgggc agcctggggc tgttcctgca gtgcgccatc 840
 35 tccctggctc tctctctggt catggaccgg ctggtgcagc gattcggcac tcgagcagtc 900
 tatttggcca gtgtggcagc tttccctgtg gctgccggtg ccacatgcct gtcccacagt 960
 gtggccgtgg tgacagcttc agccgccctc accgggttca ccttctcagc cctgcagatc 1020
 ctgccctaca cactggcctc cctctaccac cgggagaagc aggtgttctt gcccaaatac 1080
 cgaggggaca ctggagggtgc tagcagtga gacagcctga tgaccagctt cctgccaggc 1140
 40 cctaagcctg gagctccctt ccctaagga cacgtgggtg ctggaggcag tggcctgtct 1200
 ccacctccac ccgcgctctg cggggcctct gcctgtgatg tctccgtacg tgtggtgggt 1260
 ggtgagccca ccgaggccag ggtggttccg ggccggggca tctgcctgga cctcgccatc 1320
 ctggatagtg ccttctctgt gtcccagggt gcccacatcc tgtttatggg ctccattgtc 1380
 cagctcagcc agtctgtcac tgcctatatg gtgtctgccg caggcctggg tctgggtcgc 1440
 45 atttactttg ctacacaggt agtatattgac aagagcgact tggccaaata ctcagcgggt 1500
 ggacaccatc accatcacca ttaa 1524

<210> 31
 <211> 685
 50 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human P501S (amino acids 1-34 fused to 55-553)
 55 fused to 6 histidine residues

<400> 31
 Met Ala Ala Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg
 1 5 10 15
 60 Lys Ala Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val
 20 25 30

	Cys	Leu	Ala	Ala	Ala	Tyr	Val	His	Ser	Asp	Gly	Ser	Tyr	Pro	Lys	Asp
		35					40					45				
	Lys	Phe	Glu	Lys	Ile	Asn	Gly	Thr	Trp	Tyr	Tyr	Phe	Asp	Ser	Ser	Gly
	50					55					60					
5	Tyr	Met	Leu	Ala	Asp	Arg	Trp	Arg	Lys	His	Thr	Asp	Gly	Asn	Trp	Tyr
	65				70					75					80	
	Trp	Phe	Asp	Asn	Ser	Gly	Glu	Met	Ala	Thr	Gly	Trp	Lys	Lys	Ile	Ala
				85					90					95		
	Asp	Lys	Trp	Tyr	Tyr	Phe	Asn	Glu	Glu	Gly	Ala	Met	Lys	Thr	Gly	Trp
10				100					105					110		
	Val	Lys	Tyr	Lys	Asp	Thr	Trp	Tyr	Tyr	Leu	Asp	Ala	Lys	Glu	Gly	Ala
		115						120					125			
	Met	Gln	Tyr	Ile	Lys	Ala	Asn	Ser	Lys	Phe	Ile	Gly	Ile	Thr	Glu	Gly
	130						135					140				
15	Val	Met	Val	Ser	Asn	Ala	Phe	Ile	Gln	Ser	Ala	Asp	Gly	Thr	Gly	Trp
	145				150						155					160
	Tyr	Tyr	Leu	Lys	Pro	Asp	Gly	Thr	Leu	Ala	Asp	Arg	Pro	Glu	Lys	Phe
				165					170						175	
	Met	Tyr	Met	Val	Leu	Gly	Ile	Gly	Pro	Val	Leu	Gly	Leu	Val	Cys	Val
20				180					185					190		
	Pro	Leu	Leu	Gly	Ser	Ala	Ser	Asp	His	Trp	Arg	Gly	Arg	Tyr	Gly	Arg
		195						200					205			
	Arg	Arg	Pro	Phe	Ile	Trp	Ala	Leu	Ser	Leu	Gly	Ile	Leu	Leu	Ser	Leu
	210						215					220				
25	Phe	Leu	Ile	Pro	Arg	Ala	Gly	Trp	Leu	Ala	Gly	Leu	Leu	Cys	Pro	Asp
	225				230						235					240
	Pro	Arg	Pro	Leu	Glu	Leu	Ala	Leu	Leu	Ile	Leu	Gly	Val	Gly	Leu	Leu
				245						250				255		
	Asp	Phe	Cys	Gly	Gln	Val	Cys	Phe	Thr	Pro	Leu	Glu	Ala	Leu	Leu	Ser
30				260					265					270		
	Asp	Leu	Phe	Arg	Asp	Pro	Asp	His	Cys	Arg	Gln	Ala	Tyr	Ser	Val	Tyr
		275						280					285			
	Ala	Phe	Met	Ile	Ser	Leu	Gly	Gly	Cys	Leu	Gly	Tyr	Leu	Leu	Pro	Ala
	290						295					300				
35	Ile	Asp	Trp	Asp	Thr	Ser	Ala	Leu	Ala	Pro	Tyr	Leu	Gly	Thr	Gln	Glu
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				325						330					335	
	Ala	Thr	Leu	Leu	Val	Ala	Glu	Glu	Ala	Ala	Leu	Gly	Pro	Thr	Glu	Pro
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		355						360					365			
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45	His	Gln	Leu	Cys	Cys	Arg	Met	Pro	Arg	Thr	Leu	Arg	Arg	Leu	Phe	Val
	385				390						395					400
	Ala	Glu	Leu	Cys	Ser	Trp	Met	Ala	Leu	Met	Thr	Phe	Thr	Leu	Phe	Tyr
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	Thr	Asp	Phe	Val	Gly	Glu	Gly	Leu	Tyr	Gln	Gly	Val	Pro	Arg	Ala	Glu
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	Phe	Ser	Ala	Leu	Gln	Ile	Leu	Pro	Tyr	Thr	Leu	Ala	Ser	Leu	Tyr	His

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	Arg	Glu	Lys	Gln	Val	Phe	Leu	Pro	Lys	Tyr	Arg	Gly	Asp	Thr
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	Ala	Ser	Ser	Glu	Asp	Ser	Leu	Met	Thr	Ser	Phe	Leu	Pro	Gly
5	545					550					555			560
	Pro	Gly	Ala	Pro	Phe	Pro	Asn	Gly	His	Val	Gly	Ala	Gly	Gly
					565					570				575
	Leu	Leu	Pro	Pro	Pro	Pro	Ala	Leu	Cys	Gly	Ala	Ser	Ala	Cys
					580				585					590
10	Ser	Val	Arg	Val	Val	Val	Gly	Glu	Pro	Thr	Glu	Ala	Arg	Val
			595					600					605	
	Gly	Arg	Gly	Ile	Cys	Leu	Asp	Leu	Ala	Ile	Leu	Asp	Ser	Ala
		610					615					620		
	Leu	Ser	Gln	Val	Ala	Pro	Ser	Leu	Phe	Met	Gly	Ser	Ile	Val
						630					635			640
15	Ser	Gln	Ser	Val	Thr	Ala	Tyr	Met	Val	Ser	Ala	Ala	Gly	Leu
					645					650				655
	Val	Ala	Ile	Tyr	Phe	Ala	Thr	Gln	Val	Val	Phe	Asp	Lys	Ser
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<210> 32

25 <211> 2058

<212> DNA

<213> Artificial Sequence

<220>

30 <223> DNA encoding Human P501S (amino acids 1-34 fused to 55-553) fused to 6 histidine residues

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	tccgacggct	cttatccaaa	agacaagttt	gagaaaatca	atggcacttg	gtactacttt	180
	gacagtccag	gctatatgct	tgcagaccgc	tggaggaagc	acacagacgg	caactgggtac	240
	tggttcgaca	actcaggcga	aatggctaca	ggctggaaga	aaatcgctga	taagtgggtac	300
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40	tacttagacg	ctaaagaagg	cgccatgcaa	tacatcaagg	ctaactctaa	gttcattgggt	420
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catcaccatc accattaa                                     2058

<210> 33
10 <211> 671
    <212> PRT
    <213> Artificial Sequence

<220>
15 <223> St. pneum. C-LytA portion fused to P2 T helper
    epitope fused to Human P501S (amino acids 55-553)
    fused to 6 histidine residues downstream of yeast
    alphaprepro signal sequence

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    Ser Ser Ala Leu Ala Ala Ala Tyr Val His Ser Asp Gly Ser Tyr Pro
      20           25           30
25 Lys Asp Lys Phe Glu Lys Ile Asn Gly Thr Trp Tyr Tyr Phe Asp Ser
      35           40           45
    Ser Gly Tyr Met Leu Ala Asp Arg Trp Arg Lys His Thr Asp Gly Asn
      50           55           60
    Trp Tyr Trp Phe Asp Asn Ser Gly Glu Met Ala Thr Gly Trp Lys Lys
      65           70           75           80
30 Ile Ala Asp Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala Met Lys Thr
      85           90           95
    Gly Trp Val Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp Ala Lys Glu
      100          105          110
35 Gly Ala Met Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr
      115          120          125
    Glu Gly Val Met Val Ser Asn Ala Phe Ile Gln Ser Ala Asp Gly Thr
      130          135          140
    Gly Trp Tyr Tyr Leu Lys Pro Asp Gly Thr Leu Ala Asp Arg Pro Glu
      145          150          155          160
40 Lys Phe Met Tyr Met Val Leu Gly Ile Gly Pro Val Leu Gly Leu Val
      165          170          175
    Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly Arg Tyr
      180          185          190
45 Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile Leu Leu
      195          200          205
    Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu Leu Cys
      210          215          220
    Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Ile Leu Gly Val Gly
      225          230          235          240
50 Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu Ala Leu
      245          250          255
    Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala Tyr Ser
      260          265          270
55 Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr Leu Leu
      275          280          285
    Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr
      290          295          300
    Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu Thr Cys
      305          310          315          320
60 Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly Pro Thr

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325 330 335
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 340 345 350
 5 Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu Leu Pro
 355 360 365
 Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg Arg Leu
 370 375 380
 Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe Thr Leu
 385 390 395 400
 10 Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg
 405 410 415
 Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg
 420 425 430
 15 Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu Val Phe
 435 440 445
 Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val
 450 455 460
 Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys
 465 470 475 480
 20 Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu Thr Gly
 485 490 495
 Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala Ser Leu
 500 505 510
 Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly Asp Thr
 515 520 525
 25 Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu Pro Gly
 530 535 540
 Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly Gly
 545 550 555 560
 30 Ser Gly Leu Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser Ala Cys
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 Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala Arg Val
 580 585 590
 35 Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp Ser Ala
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 Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser Ile Val
 610 615 620
 Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala Gly Leu
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 <210> 34
 <211> 2477
 <212> DNA
 <213> Artificial Sequence
 50
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 <223> DNA encoding St. pneum. C-LytA portion fused to P2
 T helper epitope fused to Human P501S (amino acids
 55-553) fused to 6 histidine residues downstream
 55 of yeast alphaprepro signal sequence
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 60 aactgggtact ggttcgacaa ctcaggcgaa atggctacag gctggaagaa aatcgctgat 180
 aagtgggtact atttcaacga agaaggtgcc atgaagacag gctgggtcaa gtacaaggac 240

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40  <210> 35
    <211> 595
    <212> PRT
    <213> Artificial Sequence

45  <220>
    <223> Human P501S (amino acids 55-553) fused to 6
        histidine residues downstream of yeast alphaprepro
        signal sequence

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    Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln Ile
      20           25           30
55  Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe Asp
      35           40           45
    Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu Phe
      50           55           60
    Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val Ser
      65           70           75           80
60  Leu Glu Lys Arg Glu Ala Glu Ala Met Val Leu Gly Ile Gly Pro Val

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5	Arg	Gly	Arg	Tyr	Gly	Arg	Arg	Arg	Pro	Phe	Ile	Trp	Ala	Leu	Ser	Leu
			115					120					125			
	Gly	Ile	Leu	Leu	Ser	Leu	Phe	Leu	Ile	Pro	Arg	Ala	Gly	Trp	Leu	Ala
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	Gly	Leu	Leu	Cys	Pro	Asp	Pro	Arg	Pro	Leu	Glu	Leu	Ala	Leu	Leu	Ile
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10	Leu	Gly	Val	Gly	Leu	Leu	Asp	Phe	Cys	Gly	Gln	Val	Cys	Phe	Thr	Pro
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	Ala	Ser	Ala	Cys	Asp	Val	Ser	Val	Arg	Val	Val	Val	Gly	Glu	Pro	Thr
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	Leu	Asp	Ser	Ala	Phe	Leu	Leu	Ser	Gln	Val	Ala	Pro	Ser	Leu	Phe	Met
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	Gly	Ser	Ile	Val	Gln	Leu	Ser	Gln	Ser	Val	Thr	Ala	Tyr	Met	Val	Ser
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				565						570					575	

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10

15

20

50

55

60

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<210> 38
 <211> 2045
 35 <212> DNA
 <213> Artificial Sequence

<220>
 <223> DNA encoding codon-optimised Human P501S (amino acids 1-553)
 40 fused to St.pneum. C-LytA P2 helper epitope C-LytA

<400> 38
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 45 accgctggcg gaagcacacc gacggcaact ggtactgggt cgataactcg ggagagatgg 180
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 50 acgcctttat ccagagcgcc gacggcaccg gatggtacta cttgaagccg gacggcacc 420
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<210> 39

<211> 2105

20 <212> DNA

<213> Artificial Sequence

<220>

25 <223> DNA encoding St.pneum. C-LytA P2 helper epitope
C-Lyta fused to Human P501S (amino acids 51-553)
fused to Human P501S (amino acids 1-50) -
Codon-optimised

<400> 39

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30 gcggcgcgcg caccatggcc gccgcctacg tgcatagcga cgggagctac cccaaggaca 60
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accgctggcg gaagcacacc gacggcaact ggtactgggt cgataactcg ggagagatgg 180
ccaccggctg gaagaagatc gcggacaagt ggtactatct caacgaggag ggcgccatga 240
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35 tgcagtatat caaggccaac agcaagttca tcggcatcac cgagggaagt atggtcagca 360
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tgagcgccgc cggcctgggg ttgggtggcca tctactttgc caccaggtc gtgttcgaca 1920

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agagcgatct cgccaagtat agcgccatgg tgcagcggct gtgggtgtcc cggctgctgc 1980
gccatagaaa ggcccagttg ctgctgggtga acctgctgac ttccggactg gaggtgtgctc 2040
tggtgcccgg gatcacgtac gtgccccccc tgcctgctgga ggtgggcgtg gaggagttag 2100
gatcc 2105

5 <210> 40
  <211> 2105
  <212> DNA
  <213> Artificial Sequence

10 <220>
  <223> DNA encoding Human P501S (amino acids 1-50) fused
        to St.pneum. C-LyTA P2 helper epitope C-Lyta fused
        to Human P501S (amino acids 51-553) -
15 Codon-optimised

  <400> 40
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20 tcacgtacgt gccccccctg ctgctggagg tgggcgtgga ggagatggcc gccgcctacg 180
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ggtactatct caacgaggag ggcgccatga agaccggctg ggtgaagtat aaggacacct 420
25 ggtactacct cgacgccaaag gagggcgcca tgcagtatat caaggccaac agcaagttca 480
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gatgggtacta cttgaagccg gacggcaccc tcgcggtatc gcccgagaag ttcattgtaca 600
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gatcc 2105

55 <210> 41
  <211> 652
  <212> PRT
  <213> Artificial Sequence

60 <220>
  <223> St.pneum. C-LyTA P2 helper epitope C-Lyta fused to

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Human P501S

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10  Met Leu Ala Asp Arg Trp Arg Lys His Thr Asp Gly Asn Trp Tyr Trp
    35      40      45
    Phe Asp Asn Ser Gly Glu Met Ala Thr Gly Trp Lys Lys Ile Ala Asp
    50      55      60
    Lys Trp Tyr Tyr Phe Asn Glu Gly Ala Met Lys Thr Gly Trp Val
    65      70      75      80
    Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp Ala Lys Glu Gly Ala Met
    85      90      95
15  Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Gly Val
    100      105      110
    Met Val Ser Asn Ala Phe Ile Gln Ser Ala Asp Gly Thr Gly Trp Tyr
    115      120      125
20  Tyr Leu Lys Pro Asp Gly Thr Leu Ala Asp Arg Pro Glu Lys Phe Met
    130      135      140
    Tyr Met Val Leu Gly Ile Gly Pro Val Leu Gly Leu Val Cys Val Pro
    145      150      155      160
    Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg
    165      170      175
25  Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile Leu Leu Ser Leu Phe
    180      185      190
    Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu Leu Cys Pro Asp Pro
    195      200      205
30  Arg Pro Leu Glu Leu Ala Leu Ile Leu Gly Val Gly Leu Leu Asp
    210      215      220
    Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu Ala Leu Leu Ser Asp
    225      230      235      240
    Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala Tyr Ser Val Tyr Ala
    245      250      255
35  Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr Leu Leu Pro Ala Ile
    260      265      270
    Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu Glu
    275      280      285
40  Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu Thr Cys Val Ala Ala
    290      295      300
    Thr Leu Leu Val Ala Glu Ala Ala Leu Gly Pro Thr Glu Pro Ala
    305      310      315      320
    Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His Cys Cys Pro Cys Arg
    325      330      335
45  Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu Leu Pro Arg Leu His
    340      345      350
    Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg Arg Leu Phe Val Ala
    355      360      365
50  Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe Thr Leu Phe Tyr Thr
    370      375      380
    Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro
    385      390      395      400
    Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg Met Gly Ser
    405      410      415
55  Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu Val Phe Ser Leu Val
    420      425      430
    Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr Leu Ala
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60  Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys Leu Ser His
    450      455      460

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Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu Thr Gly Phe Thr Phe
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 Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala Ser Leu Tyr His Arg
 485 490 495
 5 Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly Asp Thr Gly Gly Ala
 500 505 510
 Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu Pro Gly Pro Lys Pro
 515 520 525
 10 Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly Gly Ser Gly Leu
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 Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser Ala Cys Asp Val Ser
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 Val Arg Val Val Val Gly Glu Pro Thr Glu Ala Arg Val Val Pro Gly
 565 570 575
 15 Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp Ser Ala Phe Leu Leu
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 595 600 605
 20 Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala Gly Leu Gly Leu Val
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25

<210> 42

<211> 1959

<212> DNA

30 <213> Artificial Sequence

<220>

 <223> DNA encoding St.pneum. C-LytA P2 helper epitope
 C-Lyta fused to Human P501S (plus his tag)

35

<400> 42

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aaatactcag cgggtgggaca ccatcaccat caccattaa 1959

10 <210> 43
    <211> 553
    <212> PRT
    <213> Homo sapiens

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20 Ala Ala Gly Ile Thr Tyr Val Pro Leu Leu Leu Glu Val Gly Val
      35           40           45
    Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly
      50           55           60
    Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly
25 65           70           75           80
    Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile
      85           90           95
    Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu
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      130          135          140
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35 145          150          155          160
    Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr
      165          170          175
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      180          185          190
40 Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu
      195          200          205
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      210          215          220
    Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His
45 225          230          235          240
    Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu
      245          250          255
    Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg
      260          265          270
50 Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe
      275          280          285
    Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val
      290          295          300
    Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly
55 305          310          315          320
    Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu
      325          330          335
    Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg
      340          345          350
60 Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala
      355          360          365

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 385 390 395 400
 5 Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly
 405 410 415
 Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu
 420 425 430
 10 Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala
 435 440 445
 Gly Gly Ser Gly Leu Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser
 450 455 460
 Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala
 465 470 475 480
 15 Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp
 485 490 495
 Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser
 500 505 510
 20 Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala
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 30 <213> Artificial Sequence
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 Human P501S
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 20 25 30
 Met Leu Ala Asp Arg Trp Arg Lys His Thr Asp Gly Asn Trp Tyr Trp
 35 40 45
 Phe Asp Asn Ser Gly Glu Met Ala Thr Gly Trp Lys Lys Ile Ala Asp
 50 55 60
 45 Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala Met Lys Thr Gly Trp Val
 65 70 75 80
 Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp Ala Lys Glu Gly Ala Met
 85 90 95
 50 Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Gly Val
 100 105 110
 Met Val Ser Asn Ala Phe Ile Gln Ser Ala Asp Gly Thr Gly Trp Tyr
 115 120 125
 Tyr Leu Lys Pro Asp Gly Thr Leu Ala Asp Arg Pro Glu Lys Phe Met
 130 135 140
 55 Tyr Met Val Leu Gly Ile Gly Pro Val Leu Gly Leu Val Cys Val Pro
 145 150 155 160
 Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg
 165 170 175
 60 Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile Leu Leu Ser Leu Phe
 180 185 190
 Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu Leu Cys Pro Asp Pro

		195				200				205						
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	Phe	Cys	Gly	Gln	Val	Cys	Phe	Thr	Pro	Leu	Glu	Ala	Leu	Leu	Ser	Asp
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	Leu	Phe	Arg	Asp	Pro	Asp	His	Cys	Arg	Gln	Ala	Tyr	Ser	Val	Tyr	Ala
					245					250					255	
	Phe	Met	Ile	Ser	Leu	Gly	Gly	Cys	Leu	Gly	Tyr	Leu	Leu	Pro	Ala	Ile
				260					265					270		
10	Asp	Trp	Asp	Thr	Ser	Ala	Leu	Ala	Pro	Tyr	Leu	Gly	Thr	Gln	Glu	Glu
			275					280					285			
	Cys	Leu	Phe	Gly	Leu	Leu	Thr	Leu	Ile	Phe	Leu	Thr	Cys	Val	Ala	Ala
		290					295					300				
	Thr	Leu	Leu	Val	Ala	Glu	Glu	Ala	Ala	Leu	Gly	Pro	Thr	Glu	Pro	Ala
15	305					310					315				320	
	Glu	Gly	Leu	Ser	Ala	Pro	Ser	Leu	Ser	Pro	His	Cys	Cys	Pro	Cys	Arg
					325					330					335	
	Ala	Arg	Leu	Ala	Phe	Arg	Asn	Leu	Gly	Ala	Leu	Leu	Pro	Arg	Leu	His
				340					345					350		
20	Gln	Leu	Cys	Cys	Arg	Met	Pro	Arg	Thr	Leu	Arg	Arg	Leu	Phe	Val	Ala
			355					360					365			
	Glu	Leu	Cys	Ser	Trp	Met	Ala	Leu	Met	Thr	Phe	Thr	Leu	Phe	Tyr	Thr
		370					375					380				
	Asp	Phe	Val	Gly	Glu	Gly	Leu	Tyr	Gln	Gly	Val	Pro	Arg	Ala	Glu	Pro
25	385					390					395				400	
	Gly	Thr	Glu	Ala	Arg	Arg	His	Tyr	Asp	Glu	Gly	Val	Arg	Met	Gly	Ser
					405					410					415	
	Leu	Gly	Leu	Phe	Leu	Gln	Cys	Ala	Ile	Ser	Leu	Val	Phe	Ser	Leu	Val
				420					425					430		
30	Met	Asp	Arg	Leu	Val	Gln	Arg	Phe	Gly	Thr	Arg	Ala	Val	Tyr	Leu	Ala
			435					440					445			
	Ser	Val	Ala	Ala	Phe	Pro	Val	Ala	Ala	Gly	Ala	Thr	Cys	Leu	Ser	His
			450				455					460				
	Ser	Val	Ala	Val	Val	Thr	Ala	Ser	Ala	Ala	Leu	Thr	Gly	Phe	Thr	Phe
35	465					470					475				480	
	Ser	Ala	Leu	Gln	Ile	Leu	Pro	Tyr	Thr	Leu	Ala	Ser	Leu	Tyr	His	Arg
					485					490					495	
	Glu	Lys	Gln	Val	Phe	Leu	Pro	Lys	Tyr	Arg	Gly	Asp	Thr	Gly	Gly	Ala
				500				505					510			
40	Ser	Ser	Glu	Asp	Ser	Leu	Met	Thr	Ser	Phe	Leu	Pro	Gly	Pro	Lys	Pro
			515					520					525			
	Gly	Ala	Pro	Phe	Pro	Asn	Gly	His	Val	Gly	Ala	Gly	Gly	Ser	Gly	Leu
			530				535						540			
	Leu	Pro	Pro	Pro	Pro	Ala	Leu	Cys	Gly	Ala	Ser	Ala	Cys	Asp	Val	Ser
45	545					550					555				560	
	Val	Arg	Val	Val	Val	Gly	Glu	Pro	Thr	Glu	Ala	Arg	Val	Val	Pro	Gly
					565					570					575	
	Arg	Gly	Ile	Cys	Leu	Asp	Leu	Ala	Ile	Leu	Asp	Ser	Ala	Phe	Leu	Leu
				580					585					590		
50	Ser	Gln	Val	Ala	Pro	Ser	Leu	Phe	Met	Gly	Ser	Ile	Val	Gln	Leu	Ser
				595					600					605		
	Gln	Ser	Val	Thr	Ala	Tyr	Met	Val	Ser	Ala	Ala	Gly	Leu	Gly	Leu	Val
		610					615						620			
	Ala	Ile	Tyr	Phe	Ala	Thr	Gln	Val	Val	Phe	Asp	Lys	Ser	Asp	Leu	Ala
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	Lys	Tyr	Ser	Ala												

60 <210> 45
 <211> 644

<212> PRT

<213> Artificial Sequence

<220>

- 5 <223> Codon-optimised hybrid protein between St.pneum. C-LyTA P2
 helper epitope C-Lyta fused to Human P501S
 amino acids 51-553)

<400> 45

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    Phe Glu Lys Ile Asn Gly Thr Trp Tyr Tyr Phe Asp Ser Ser Gly Tyr
        20      25      30
15 Met Leu Ala Asp Arg Trp Arg Lys His Thr Asp Gly Asn Trp Tyr Trp
    35      40      45
    Phe Asp Asn Ser Gly Glu Met Ala Thr Gly Trp Lys Lys Ile Ala Asp
    50      55      60
    Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala Met Lys Thr Gly Trp Val
    65      70      75      80
20 Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp Ala Lys Glu Gly Ala Met
    85      90      95
    Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Gly Val
    100      105      110
25 Met Val Ser Asn Ala Phe Ile Gln Ser Ala Asp Gly Thr Gly Trp Tyr
    115      120      125
    Tyr Leu Lys Pro Asp Gly Thr Leu Ala Asp Arg Pro Glu Lys Phe Met
    130      135      140
    Tyr Met Val Leu Gly Ile Gly Pro Val Leu Gly Leu Val Cys Val Pro
    145      150      155      160
30 Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg
    165      170      175
    Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile Leu Leu Ser Leu Phe
    180      185      190
35 Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu Leu Cys Pro Asp Pro
    195      200      205
    Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly Val Gly Leu Leu Asp
    210      215      220
    Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu Ala Leu Leu Ser Asp
    225      230      235      240
40 Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala Tyr Ser Val Tyr Ala
    245      250      255
    Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr Leu Leu Pro Ala Ile
    260      265      270
45 Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu Glu
    275      280      285
    Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu Thr Cys Val Ala Ala
    290      295      300
    Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly Pro Thr Glu Pro Ala
    305      310      315      320
50 Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His Cys Cys Pro Cys Arg
    325      330      335
    Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu Leu Pro Arg Leu His
    340      345      350
55 Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg Arg Leu Phe Val Ala
    355      360      365
    Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe Thr Leu Phe Tyr Thr
    370      375      380
    Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro
    385      390      395      400
60 Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg Met Gly Ser
    405      410      415

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Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu Val Phe Ser Leu Val
 420 425 430
 Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr Leu Ala
 435 440 445
 5 Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys Leu Ser His
 450 455 460
 Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu Thr Gly Phe Thr Phe
 465 470 475 480
 10 Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala Ser Leu Tyr His Arg
 485 490 495
 Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly Asp Thr Gly Gly Ala
 500 505 510
 Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu Pro Gly Pro Lys Pro
 515 520 525
 15 Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly Gly Ser Gly Leu
 530 535 540
 Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser Ala Cys Asp Val Ser
 545 550 555 560
 Val Arg Val Val Val Gly Glu Pro Thr Glu Ala Arg Val Val Pro Gly
 565 570 575
 20 Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp Ser Ala Phe Leu Leu
 580 585 590
 Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser Ile Val Gln Leu Ser
 595 600 605
 25 Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala Gly Leu Gly Leu Val
 610 615 620
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 Lys Tyr Ser Ala

<210> 46
 <211> 694
 35 <212> PRT
 <213> Artificial Sequence

<220>
 <223> St.pneum. C-LytA P2 helper epitope C-Lyta fused to
 40 Human P501S (amino acids 1-553)- codon optimised

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 Met Ala Ala Ala Tyr Val His Ser Asp Gly Ser Tyr Pro Lys Asp Lys
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 45 Phe Glu Lys Ile Asn Gly Thr Trp Tyr Tyr Phe Asp Ser Ser Gly Tyr
 20 25 30
 Met Leu Ala Asp Arg Trp Arg Lys His Thr Asp Gly Asn Trp Tyr Trp
 35 40 45
 Phe Asp Asn Ser Gly Glu Met Ala Thr Gly Trp Lys Lys Ile Ala Asp
 50 55 60
 Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala Met Lys Thr Gly Trp Val
 65 70 75 80
 Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp Ala Lys Glu Gly Ala Met
 85 90 95
 55 Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Gly Val
 100 105 110
 Met Val Ser Asn Ala Phe Ile Gln Ser Ala Asp Gly Thr Gly Trp Tyr
 115 120 125
 Tyr Leu Lys Pro Asp Gly Thr Leu Ala Asp Arg Pro Glu Met Val Gln
 130 135 140
 60 Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala Gln Leu Leu

	145				150				155				160
	Leu	Val	Asn	Leu	Leu	Thr	Phe	Gly	Leu	Glu	Val	Cys	Leu
					165					170			175
	Ile	Thr	Tyr	Val	Pro	Pro	Leu	Leu	Leu	Glu	Val	Gly	Val
5				180					185				190
	Phe	Met	Thr	Met	Val	Leu	Gly	Ile	Gly	Pro	Val	Leu	Gly
			195					200				205	
	Val	Pro	Leu	Leu	Gly	Ser	Ala	Ser	Asp	His	Trp	Arg	Gly
		210					215				220		
10	Arg	Arg	Arg	Pro	Phe	Ile	Trp	Ala	Leu	Ser	Leu	Gly	Ile
		225				230					235		
	Leu	Phe	Leu	Ile	Pro	Arg	Ala	Gly	Trp	Leu	Ala	Gly	Leu
				245					250				255
	Asp	Pro	Arg	Pro	Leu	Glu	Leu	Ala	Leu	Leu	Ile	Leu	Gly
15				260					265				270
	Leu	Asp	Phe	Cys	Gly	Gln	Val	Cys	Phe	Thr	Pro	Leu	Glu
			275					280				285	
	Ser	Asp	Leu	Phe	Arg	Asp	Pro	Asp	His	Cys	Arg	Gln	Ala
		290				295					300		
20	Tyr	Ala	Phe	Met	Ile	Ser	Leu	Gly	Gly	Cys	Leu	Gly	Tyr
		305				310					315		
	Ala	Ile	Asp	Trp	Asp	Thr	Ser	Ala	Leu	Ala	Pro	Tyr	Leu
				325					330				335
	Glu	Glu	Cys	Leu	Phe	Gly	Leu	Leu	Thr	Leu	Ile	Phe	Leu
25				340					345				350
	Ala	Ala	Thr	Leu	Leu	Val	Ala	Glu	Glu	Ala	Ala	Leu	Gly
			355					360				365	
	Pro	Ala	Glu	Gly	Leu	Ser	Ala	Pro	Ser	Leu	Ser	Pro	His
		370				375					380		
30	Cys	Arg	Ala	Arg	Leu	Ala	Phe	Arg	Asn	Leu	Gly	Ala	Leu
		385				390					395		
	Leu	His	Gln	Leu	Cys	Cys	Arg	Met	Pro	Arg	Thr	Leu	Arg
				405					410				415
	Val	Ala	Glu	Leu	Cys	Ser	Trp	Met	Ala	Leu	Met	Thr	Phe
35				420					425				430
	Tyr	Thr	Asp	Phe	Val	Gly	Glu	Gly	Leu	Tyr	Gln	Gly	Val
			435					440				445	
	Glu	Pro	Gly	Thr	Glu	Ala	Arg	Arg	His	Tyr	Asp	Glu	Gly
		450				455					460		
40	Gly	Ser	Leu	Gly	Leu	Phe	Leu	Gln	Cys	Ala	Ile	Ser	Leu
					470					475			480
	Leu	Val	Met	Asp	Arg	Leu	Val	Gln	Arg	Phe	Gly	Thr	Arg
				485					490				495
	Leu	Ala	Ser	Val	Ala	Ala	Phe	Pro	Val	Ala	Ala	Gly	Ala
45				500					505				510
	Ser	His	Ser	Val	Ala	Val	Val	Thr	Ala	Ser	Ala	Ala	Leu
			515					520				525	
	Thr	Phe	Ser	Ala	Leu	Gln	Ile	Leu	Pro	Tyr	Thr	Leu	Ala
		530				535					540		
50	His	Arg	Glu	Lys	Gln	Val	Phe	Leu	Pro	Lys	Tyr	Arg	Gly
		545				550					555		
	Gly	Ala	Ser	Ser	Glu	Asp	Ser	Leu	Met	Thr	Ser	Phe	Leu
				565					570				575
	Lys	Pro	Gly	Ala	Pro	Phe	Pro	Asn	Gly	His	Val	Gly	Ala
55				580					585				590
	Gly	Leu	Leu	Pro	Pro	Pro	Pro	Ala	Leu	Cys	Gly	Ala	Ser
			595					600				605	
	Val	Ser	Val	Arg	Val	Val	Val	Gly	Glu	Pro	Thr	Glu	Ala
		610				615					620		
60	Pro	Gly	Arg	Gly	Ile	Cys	Leu	Asp	Leu	Ala	Ile	Leu	Asp
		625				630				635			640

Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser Ile Val Gln
 645 650 655
 Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala Gly Leu Gly
 660 665 670
 5 Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp Lys Ser Asp
 675 680 685
 Leu Ala Lys Tyr Ser Ala
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 10 <210> 47
 <211> 694
 <212> PRT
 <213> Artificial Sequence

 15 <220>
 <223> St.pneum. C-LyTA P2 helper epitope C-LyTA fused to
 Human P501S (amino acids 51-553) fused to Human
 P501S (amino acids 1-50) - codon-optimised

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 25 20 25 30
 Met Leu Ala Asp Arg Trp Arg Lys His Thr Asp Gly Asn Trp Tyr Trp
 35 40 45
 Phe Asp Asn Ser Gly Glu Met Ala Thr Gly Trp Lys Lys Ile Ala Asp
 50 55 60
 30 Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala Met Lys Thr Gly Trp Val
 65 70 75 80
 Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp Ala Lys Glu Gly Ala Met
 85 90 95
 Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Gly Val
 35 100 105 110
 Met Val Ser Asn Ala Phe Ile Gln Ser Ala Asp Gly Thr Gly Trp Tyr
 115 120 125
 Tyr Leu Lys Pro Asp Gly Thr Leu Ala Asp Arg Pro Glu Lys Phe Met
 130 135 140
 40 Tyr Met Val Leu Gly Ile Gly Pro Val Leu Gly Leu Val Cys Val Pro
 145 150 155 160
 Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg
 165 170 175
 Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile Leu Leu Ser Leu Phe
 45 180 185 190
 Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu Leu Cys Pro Asp Pro
 195 200 205
 Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly Val Gly Leu Leu Asp
 210 215 220
 50 Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu Ala Leu Leu Ser Asp
 225 230 235 240
 Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala Tyr Ser Val Tyr Ala
 245 250 255
 Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr Leu Leu Pro Ala Ile
 55 260 265 270
 Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu Glu
 275 280 285
 Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu Thr Cys Val Ala Ala
 290 295 300
 60 Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly Pro Thr Glu Pro Ala
 305 310 315 320

Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His Cys Cys Pro Cys Arg
 325 330 335
 Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu Leu Pro Arg Leu His
 340 345 350
 5 Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg Arg Leu Phe Val Ala
 355 360 365
 Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe Thr Leu Phe Tyr Thr
 370 375 380
 10 Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro
 385 390 395 400
 Gly Thr Glu Ala Arg His Tyr Asp Glu Gly Val Arg Met Gly Ser
 405 410 415
 Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu Val Phe Ser Leu Val
 420 425 430
 15 Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr Leu Ala
 435 440 445
 Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys Leu Ser His
 450 455 460
 20 Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu Thr Gly Phe Thr Phe
 465 470 475 480
 Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala Ser Leu Tyr His Arg
 485 490 495
 Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly Asp Thr Gly Gly Ala
 500 505 510
 25 Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu Pro Gly Pro Lys Pro
 515 520 525
 Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly Gly Ser Gly Leu
 530 535 540
 30 Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser Ala Cys Asp Val Ser
 545 550 555 560
 Val Arg Val Val Val Gly Glu Pro Thr Glu Ala Arg Val Val Pro Gly
 565 570 575
 Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp Ser Ala Phe Leu Leu
 580 585 590
 35 Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser Ile Val Gln Leu Ser
 595 600 605
 Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala Gly Leu Gly Leu Val
 610 615 620
 40 Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp Lys Ser Asp Leu Ala
 625 630 635 640
 Lys Tyr Ser Ala Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg
 645 650 655
 His Arg Lys Ala Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu
 660 665 670
 45 Glu Val Cys Leu Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu
 675 680 685
 Glu Val Gly Val Glu Glu
 690

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<210> 48
 <211> 694
 <212> PRT
 <213> Artificial Sequence

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<220>
 <223> Human P501S (amino acids 1-50) fused to St.pneum.
 C-LytA P2 helper epitope C-Lyta fused to Human
 P501S (amino acids 51-553) - codon optimised

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<400> 48

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	Gln	Leu	Leu	Leu	Val	Asn	Leu	Leu	Thr	Phe	Gly	Leu	Glu	Val	Cys	Leu
				20					25					30		
5	Ala	Ala	Gly	Ile	Thr	Tyr	Val	Pro	Pro	Leu	Leu	Leu	Glu	Val	Gly	Val
			35					40					45			
	Glu	Glu	Met	Ala	Ala	Ala	Tyr	Val	His	Ser	Asp	Gly	Ser	Tyr	Pro	Lys
		50						55				60				
	Asp	Lys	Phe	Glu	Lys	Ile	Asn	Gly	Thr	Trp	Tyr	Tyr	Phe	Asp	Ser	Ser
10	65					70						75				80
	Gly	Tyr	Met	Leu	Ala	Asp	Arg	Trp	Arg	Lys	His	Thr	Asp	Gly	Asn	Trp
				85						90					95	
	Tyr	Trp	Phe	Asp	Asn	Ser	Gly	Glu	Met	Ala	Thr	Gly	Trp	Lys	Lys	Ile
				100					105					110		
15	Ala	Asp	Lys	Trp	Tyr	Tyr	Phe	Asn	Glu	Glu	Gly	Ala	Met	Lys	Thr	Gly
			115					120					125			
	Trp	Val	Lys	Tyr	Lys	Asp	Thr	Trp	Tyr	Tyr	Leu	Asp	Ala	Lys	Glu	Gly
		130					135					140				
	Ala	Met	Gln	Tyr	Ile	Lys	Ala	Asn	Ser	Lys	Phe	Ile	Gly	Ile	Thr	Glu
20	145					150						155				160
	Gly	Val	Met	Val	Ser	Asn	Ala	Phe	Ile	Gln	Ser	Ala	Asp	Gly	Thr	Gly
				165						170					175	
	Trp	Tyr	Tyr	Leu	Lys	Pro	Asp	Gly	Thr	Leu	Ala	Asp	Arg	Pro	Glu	Lys
				180					185					190		
25	Phe	Met	Tyr	Met	Val	Leu	Gly	Ile	Gly	Pro	Val	Leu	Gly	Leu	Val	Cys
			195					200					205			
	Val	Pro	Leu	Leu	Gly	Ser	Ala	Ser	Asp	His	Trp	Arg	Gly	Arg	Tyr	Gly
		210					215					220				
30	Arg	Arg	Arg	Pro	Phe	Ile	Trp	Ala	Leu	Ser	Leu	Gly	Ile	Leu	Leu	Ser
		225				230						235				240
	Leu	Phe	Leu	Ile	Pro	Arg	Ala	Gly	Trp	Leu	Ala	Gly	Leu	Leu	Cys	Pro
				245						250					255	
	Asp	Pro	Arg	Pro	Leu	Glu	Leu	Ala	Leu	Leu	Ile	Leu	Gly	Val	Gly	Leu
				260					265					270		
35	Leu	Asp	Phe	Cys	Gly	Gln	Val	Cys	Phe	Thr	Pro	Leu	Glu	Ala	Leu	Leu
			275						280					285		
	Ser	Asp	Leu	Phe	Arg	Asp	Pro	Asp	His	Cys	Arg	Gln	Ala	Tyr	Ser	Val
		290					295					300				
	Tyr	Ala	Phe	Met	Ile	Ser	Leu	Gly	Gly	Cys	Leu	Gly	Tyr	Leu	Leu	Pro
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	Ala	Ile	Asp	Trp	Asp	Thr	Ser	Ala	Leu	Ala	Pro	Tyr	Leu	Gly	Thr	Gln
				325						330					335	
	Glu	Glu	Cys	Leu	Phe	Gly	Leu	Leu	Thr	Leu	Ile	Phe	Leu	Thr	Cys	Val
				340					345				350			
45	Ala	Ala	Thr	Leu	Leu	Val	Ala	Glu	Glu	Ala	Ala	Leu	Gly	Pro	Thr	Glu
			355					360					365			
	Pro	Ala	Glu	Gly	Leu	Ser	Ala	Pro	Ser	Leu	Ser	Pro	His	Cys	Cys	Pro
		370					375					380				
	Cys	Arg	Ala	Arg	Leu	Ala	Phe	Arg	Asn	Leu	Gly	Ala	Leu	Leu	Pro	Arg
50	385					390					395					400
	Leu	His	Gln	Leu	Cys	Arg	Met	Pro	Arg	Thr	Leu	Arg	Arg	Leu	Phe	
				405					410					415		
	Val	Ala	Glu	Leu	Cys	Ser	Trp	Met	Ala	Leu	Met	Thr	Phe	Thr	Leu	Phe
				420					425					430		
55	Tyr	Thr	Asp	Phe	Val	Gly	Glu	Gly	Leu	Tyr	Gln	Gly	Val	Pro	Arg	Ala
			435					440					445			
	Glu	Pro	Gly	Thr	Glu	Ala	Arg	Arg	His	Tyr	Asp	Glu	Gly	Val	Arg	Met
		450					455					460				
	Gly	Ser	Leu	Gly	Leu	Phe	Leu	Gln	Cys	Ala	Ile	Ser	Leu	Val	Phe	Ser
60	465					470					475					480
	Leu	Val	Met	Asp	Arg	Leu	Val	Gln	Arg	Phe	Gly	Thr	Arg	Ala	Val	Tyr

485 490 495
 Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys Leu
 500 505 510
 Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu Thr Gly Phe
 515 520 525
 5 Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala Ser Leu Tyr
 530 535 540
 His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly Asp Thr Gly
 545 550 555 560
 10 Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu Pro Gly Pro
 565 570 575
 Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly Gly Ser
 580 585 590
 15 Gly Leu Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser Ala Cys Asp
 595 600 605
 Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala Arg Val Val
 610 615 620
 Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp Ser Ala Phe
 625 630 635 640
 20 Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser Ile Val Gln
 645 650 655
 Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala Gly Leu Gly
 660 665 670
 25 Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp Lys Ser Asp
 675 680 685
 Leu Ala Lys Tyr Ser Ala
 690

 30 <210> 49
 <211> 1971
 <212> DNA
 <213> Artificial Sequence

 35 <220>
 <223> DNA encoding Human MUC-1 fused to St.pneum. C-LytA
 P2 helper epitope C-LytA

 <400> 49
 40 atgacaccgg gcaccagtc tcttttcttc ctgctgctgc tcttcacagt gcttacagtt 60
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 cagagaagtt cagtgccag ctctactgag aagaatgctg tgagtatgac cagcagcgta 180
 ctctccagcc acagccccgg ttcaggctcc tccaccactc agggacagga tgtcactctg 240
 gccccggcca cggaaccagc ttcaggttca gctgccacct ggggacagga tgtcacctcg 300
 45 gtccagtc caaggccagc cctgggctcc accaccccg cagcccacga tgtcacctca 360
 gccccggaca acaagccagc cccgggctcc accgcccccc cagcccacgg tgtcacctcg 420
 gccccggaca ccaggccgccc cccgggctcc accgcccccc cagcccacgg tgtcacctcg 480
 gccccggaca ccaggccgccc cccgggctcc accgcccccc cagcccacgg tgtcacctcg 540
 gccccggaca ccaggccgccc cccgggctcc accgcccccc cagcccacgg tgtcacctcg 600
 50 gccccggaca acaggcccg cttggcgctcc accgcccccc cagtccacaa tgtcacctcg 660
 gcctcaggct ctgcatcagg ctccagcttct actctggtgc acaacggcac ctctgccagg 720
 gctaccacaa cccagccag caagagcact ccattctcaa tcccagcca ccactctgat 780
 actcctacca ccttgccag ccatagcacc aagactgatg ccagtagcac tcaccatagc 840
 acgggtacctc ctctcacctc ctccaatcac agcacttctc cccagttgtc tactgggggtc 900
 55 tctttctttt tctgtcttt tcaatttca aacctccagt ttaattcctc tctggaagat 960
 cccagcaccg actactacca agagctgcag agagacattt ctgaaatgtt tttgcagatt 1020
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 gtacaattga ctctggcctt ccgagaaggt accatcaatg tccacgacgt ggagacacag 1140
 ttcaatcagt ataaaacgga agcagcctct cgatataacc tgacgatctc agacgtcagc 1200
 60 gtgagtgatg tgccatttcc tttctctgcc cagtctgggg ctgggggtgcc aggctggggc 1260
 atcgcgctgc tgggtgctggt ctgtgttctg gttgcgctgg ccattgtcta tctcattgcc 1320

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ttggctgtct gtcagtgcgc ccgaaagaac tacgggcagc tggacatctt tccagcccgg 1380
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5 gtacattccg acggctctta tccaaaagac aagtgtgaga aaatcaatgg cacttggtac 1620
tacttttgaca gttcaggcta tatgcttgca gaccgctgga ggaagcacac agacggcaac 1680
tggtactggt tcgacaactc aggcgaaatg gctacaggct ggaagaaaat cgctgataag 1740
tggtactatt tcaacgaaga aggtgccatg aagacaggct gggtaagta caaggacact 1800
tggtactact tagacgctaa agaaggcgcc atgcaataca tcaaggctaa ctctaagttc 1860
10 attggtatca ctgaaggcgt catggtatca aatgccttta tccagtcagc ggacggaaca 1920
ggctggtact acctcaaacc agacggaaca ctggcagaca ggccagaatg a 1971

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<210> 50

<211> 656

15 <212> PRT

<213> Artificial Sequence

<220>

20 <223> Human MUC-1 fused to St.pneum. C-Lyta P2 helper
epitope C-Lyta

<400> 50

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25 Val Leu Thr Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly
      20      25      30
Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
      35      40      45
30 Thr Glu Lys Asn Ala Val Ser Met Thr Ser Ser Val Leu Ser Ser His
      50      55      60
Ser Pro Gly Ser Gly Ser Ser Thr Thr Gln Gly Gln Asp Val Thr Leu
65      70      75      80
Ala Pro Ala Thr Glu Pro Ala Ser Gly Ser Ala Ala Thr Trp Gly Gln
      85      90      95
35 Asp Val Thr Ser Val Pro Val Thr Arg Pro Ala Leu Gly Ser Thr Thr
      100      105      110
Pro Pro Ala His Asp Val Thr Ser Ala Pro Asp Asn Lys Pro Ala Pro
      115      120      125
40 Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
      130      135      140
Arg Pro Pro Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser
145      150      155      160
Ala Pro Asp Thr Arg Pro Pro Pro Gly Ser Thr Ala Pro Ala Ala His
      165      170      175
45 Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala
      180      185      190
Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Asn Arg Pro Ala Leu
      195      200      205
50 Ala Ser Thr Ala Pro Pro Val His Asn Val Thr Ser Ala Ser Gly Ser
      210      215      220
Ala Ser Gly Ser Ala Ser Thr Leu Val His Asn Gly Thr Ser Ala Arg
225      230      235      240
Ala Thr Thr Thr Pro Ala Ser Lys Ser Thr Pro Phe Ser Ile Pro Ser
      245      250      255
55 His His Ser Asp Thr Pro Thr Thr Leu Ala Ser His Ser Thr Lys Thr
      260      265      270
Asp Ala Ser Ser Thr His His Ser Thr Val Pro Pro Leu Thr Ser Ser
      275      280      285
60 Asn His Ser Thr Ser Pro Gln Leu Ser Thr Gly Val Ser Phe Phe Phe
      290      295      300
Leu Ser Phe His Ile Ser Asn Leu Gln Phe Asn Ser Ser Leu Glu Asp

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37

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atcaaggcta actctaagtt cattgggtatc actgaaggcg tcatgggtatc aaatgccttt 420
atccagtcag cggacggaac aggcctgggtac tacctcaaac cagacggaac actggcagac 480
aggccagaaa tgacaccggg caccagtcct cctttcttcc tgctgctgct cctcacagtg 540
cttacagttg ttacaggttc tgggtcatgca agctctaccc caggtggaga aaaggagact 600
5 tgcggctaccc agagaagttc agtgcccagc tctactgaga agaatgctgt gagtatgacc 660
agcagcgtac tctccagcca cagccccggt tcaggctcct ccaccactca gggacaggat 720
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gtcacctcgg tcccagtcac caggccagcc ctgggctcca ccaccccgcc agcccacgat 840
gtcacctcag ccccgacaaa caagccagcc cggggtcca ccgccccccc agcccacggt 900
10 gtcacctcgg ccccgacac caggccgccc ccgggctcca ccgccccccc agcccacggt 960
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25 ctcattgcct tggctgtctg tcagtgcgcg cgaaagaact acgggcagct ggacatcttt 1860
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tatgtgcccc ctagcagtag cgatcgtagc ccctatgaga aggtttctgc aggtaatggt 1980
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30 <210> 52
    <211> 678
    <212> PRT
    <213> Artificial Sequence

35 <220>
    <223> St.pneum. C-LytA P2 helper epitope C-Lyta fused
        to Human MUC-1

40 <400> 52
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
  1          5          10          15
Val His Ser Gln Val Gln Met Ala Ala Tyr Val His Ser Asp Gly
  20          25          30
Ser Tyr Pro Lys Asp Lys Phe Glu Lys Ile Asn Gly Thr Trp Tyr Tyr
45 35          40          45
Phe Asp Ser Ser Gly Tyr Met Leu Ala Asp Arg Trp Arg Lys His Thr
  50          55          60
Asp Gly Asn Trp Tyr Trp Phe Asp Asn Ser Gly Glu Met Ala Thr Gly
  65          70          75          80
50 Trp Lys Lys Ile Ala Asp Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala
  85          90          95
Met Lys Thr Gly Trp Val Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp
  100          105          110
Ala Lys Glu Gly Ala Met Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile
55 115          120          125
Gly Ile Thr Glu Gly Val Met Val Ser Asn Ala Phe Ile Gln Ser Ala
  130          135          140
Asp Gly Thr Gly Trp Tyr Tyr Leu Lys Pro Asp Gly Thr Leu Ala Asp
145 150          155          160
60 Arg Pro Glu Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu
  165          170          175

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	Leu	Leu	Thr	Val	Leu	Thr	Val	Val	Thr	Gly	Ser	Gly	His	Ala	Ser	Ser
				180					185					190		
	Thr	Pro	Gly	Gly	Glu	Lys	Glu	Thr	Ser	Ala	Thr	Gln	Arg	Ser	Ser	Val
			195					200					205			
5	Pro	Ser	Ser	Thr	Glu	Lys	Asn	Ala	Val	Ser	Met	Thr	Ser	Ser	Val	Leu
		210					215					220				
	Ser	Ser	His	Ser	Pro	Gly	Ser	Gly	Ser	Ser	Thr	Thr	Gln	Gly	Gln	Asp
		225				230					235					240
	Val	Thr	Leu	Ala	Pro	Ala	Thr	Glu	Pro	Ala	Ser	Gly	Ser	Ala	Ala	Thr
10					245					250					255	
	Trp	Gly	Gln	Asp	Val	Thr	Ser	Val	Pro	Val	Thr	Arg	Pro	Ala	Leu	Gly
				260					265					270		
	Ser	Thr	Thr	Pro	Pro	Ala	His	Asp	Val	Thr	Ser	Ala	Pro	Asp	Asn	Lys
			275					280					285			
15	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala
		290					295					300				
	Pro	Asp	Thr	Arg	Pro	Pro	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly
		305				310					315					320
	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Pro	Pro	Gly	Ser	Thr	Ala	Pro
20					325					330					335	
	Ala	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly
				340					345					350		
	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Asn	Arg
			355					360					365			
25	Pro	Ala	Leu	Ala	Ser	Thr	Ala	Pro	Pro	Val	His	Asn	Val	Thr	Ser	Ala
		370					375					380				
	Ser	Gly	Ser	Ala	Ser	Gly	Ser	Ala	Ser	Thr	Leu	Val	His	Asn	Gly	Thr
		385				390					395					400
	Ser	Ala	Arg	Ala	Thr	Thr	Pro	Ala	Ser	Lys	Ser	Thr	Pro	Phe	Ser	
30					405				410					415		
	Ile	Pro	Ser	His	His	Ser	Asp	Thr	Pro	Thr	Thr	Leu	Ala	Ser	His	Ser
				420					425					430		
	Thr	Lys	Thr	Asp	Ala	Ser	Ser	Thr	His	His	Ser	Thr	Val	Pro	Pro	Leu
			435					440					445			
35	Thr	Ser	Ser	Asn	His	Ser	Thr	Ser	Pro	Gln	Leu	Ser	Thr	Gly	Val	Ser
		450					455					460				
	Phe	Phe	Phe	Leu	Ser	Phe	His	Ile	Ser	Asn	Leu	Gln	Phe	Asn	Ser	Ser
		465				470					475					480
	Leu	Glu	Asp	Pro	Ser	Thr	Asp	Tyr	Tyr	Gln	Glu	Leu	Gln	Arg	Asp	Ile
40					485					490					495	
	Ser	Glu	Met	Phe	Leu	Gln	Ile	Tyr	Lys	Gln	Gly	Gly	Phe	Leu	Gly	Leu
				500					505					510		
	Ser	Asn	Ile	Lys	Phe	Arg	Pro	Gly	Ser	Val	Val	Val	Gln	Leu	Thr	Leu
			515					520					525			
45	Ala	Phe	Arg	Glu	Gly	Thr	Ile	Asn	Val	His	Asp	Val	Glu	Thr	Gln	Phe
		530					535					540				
	Asn	Gln	Tyr	Lys	Thr	Glu	Ala	Ala	Ser	Arg	Tyr	Asn	Leu	Thr	Ile	Ser
		545				550					555					560
	Asp	Val	Ser	Val	Ser	Asp	Val	Pro	Phe	Pro	Phe	Ser	Ala	Gln	Ser	Gly
50					565					570					575	
	Ala	Gly	Val	Pro	Gly	Trp	Gly	Ile	Ala	Leu	Leu	Val	Leu	Val	Cys	Val
				580					585					590		
	Leu	Val	Ala	Leu	Ala	Ile	Val	Tyr	Leu	Ile	Ala	Leu	Ala	Val	Cys	Gln
			595					600					605			
55	Cys	Arg	Arg	Lys	Asn	Tyr	Gly	Gln	Leu	Asp	Ile	Phe	Pro	Ala	Arg	Asp
		610					615					620				
	Thr	Tyr	His	Pro	Met	Ser	Glu	Tyr	Pro	Thr	Tyr	His	Thr	His	Gly	Arg
		625				630					635					640
	Tyr	Val	Pro	Pro	Ser	Ser	Thr	Asp	Arg	Ser	Pro	Tyr	Glu	Lys	Val	Ser
60					645					650					655	
	Ala	Gly	Asn	Gly	Gly	Ser	Ser	Leu	Ser	Tyr	Thr	Asn	Pro	Ala	Val	Ala

WO 03/104272

PCT/EP03/06096

Ala Thr Ser Ala Asn Leu
675

665

670

5